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Listing of Claims:

The following listing of claims replaces all prior versions and listings of claims in the application.

1. - 57. (Canceled)

58. (New) A method for altering the glycosylation profile of a polypeptide of interest, the method comprising:

a) preparing a nucleic acid comprising a nucleotide sequence encoding a peptide- extended polypeptide with the primary structure $\text{NH}_2\text{-X-Pp-COOH}$, wherein

NH_2 and COOH represent the N-terminus and the C-terminus of the peptide-extended polypeptide, respectively;

X is a peptide addition 1-30 amino acids in length which comprises or contributes to an *in vivo* glycosylation site; and

Pp is the polypeptide of interest; and

b) expressing the nucleic acid in a glycosylating host cell to provide a peptide-extended glycosylated polypeptide;

wherein the peptide-extended glycosylated polypeptide exhibits an altered glycosylation pattern compared to that of the polypeptide of interest when expressed under the same conditions.

59. (New) The method of claim 58, further comprising:

c) recovering the peptide-extended glycosylated polypeptide.

60. (New) The method of claim 58, wherein X comprises or contributes to an *in vivo* N-glycosylation site.

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61. (New) The method of claim 60, wherein X is of the formula:



X_1 is absent or comprises at least one amino acid;

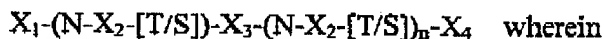
X_2 is any one amino acid except proline;

Z is absent or comprises at least one amino acid;

N is asparagine; and

[T/S]/C is threonine, serine, or cysteine.

62. (New) The method of claim 61, wherein X is of the formula:



X_1 is absent, or is any 1, 2, 3, or 4 amino acids;

X_2 is any one amino acid except proline;

X_3 is absent, or is any 1, 2, 3, or 4 amino acids;

X_4 is absent, or is any 1, 2, 3, or 4 amino acids;

n is an integer between 0 and 6; N is asparagine; and [T/S] is threonine or serine.

63. (New) The method of claim 61, wherein

X_2 is isoleucine, alanine, glycine, valine, or serine.

64. (New) The method of claim 58, wherein the glycosylating host cell is a fungal cell, an insect cell, a mammalian cell, or a plant cell.

65. (New) The method of claim 58, further comprising:

reacting the peptide-extended glycosylated polypeptide with a non-peptide moiety which differs from an oligosaccharide moiety, under conditions suitable to covalently attach at least one non-peptide moiety to an attachment group of the polypeptide.

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66. (New) A method of identifying a peptide-extended glycosylated polypeptide with an improved property relative to a polypeptide of interest, the method comprising:

a) preparing one or more recombinant nucleic acids by subjecting a nucleotide sequence encoding the polypeptide of interest to elongation mutagenesis such that the resulting one or more recombinant nucleic acids encode one or more peptide-extended polypeptides according to the formula $\text{NH}_2\text{-X-Pp-COOH}$, wherein

NH_2 and COOH represent the N-terminus and the C-terminus of the peptide-extended polypeptide, respectively;

X is a peptide addition 1-30 amino acids in length which comprises or contributes to an *in vivo* glycosylation site; and

Pp is the polypeptide of interest;

b) expressing the one or more recombinant nucleic acids in a glycosylating host cell to provide one or more peptide-extended glycosylated polypeptides, wherein the one or more peptide-extended glycosylated polypeptides exhibit an altered glycosylation pattern compared to the polypeptide of interest; and

c) screening or selecting the one or more peptide-extended glycosylated polypeptides to identify at least one peptide-extended glycosylated polypeptide with the improved property relative to the polypeptide of interest.

67. (New) The method of claim 66, further comprising:

d) recovering the peptide-extended glycosylated polypeptide with the improved property.

68. (New) The method of claim 66, wherein the nucleotide sequence encoding the peptide addition X is subjected to random mutagenesis.

69. (New) A method of making a peptide-extended glycosylated polypeptide with an improved property relative to a polypeptide of interest, the method comprising:

a) carrying out the method of claim 66 to identify a peptide-extended glycosylated polypeptide with an improved property relative to a polypeptide of interest;

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b) preparing a nucleic acid which encodes the peptide-extended glycosylated polypeptide identified in a); and

c) expressing the nucleic acid in a glycosylating host cell.

70. (New) The method of claim 69, further comprising:

d) recovering the peptide-extended glycosylated polypeptide.

71. (New) The method of claim 69, further comprising:

reacting the peptide-extended glycosylated polypeptide with a non-peptide moiety which differs from an oligosaccharide moiety, under conditions suitable to covalently attach at least one non-peptide moiety to an attachment group of the polypeptide.

72. (New) The method of claim 66, wherein the improved property relative to the polypeptide of interest is selected from the group consisting of:

increased affinity for a carbohydrate receptor; increased serum half-life; increased functional *in vivo* half-life; reduced renal clearance; reduced immunogenicity; increased resistance to proteolytic cleavage; improved targeting to lysosomes, macrophages and/or other subpopulations of human cells; improved stability in production; improved shelf life; improved formulation; improved purification; improved solubility; and improved expression.